

ENTERED



1635

RAW SEQUENCE LISTING

DATE: 05/22/2002

PATENT APPLICATION: US/09/600,358A

TIME: 13:23:40

Input Set : A:\92906-2 seq 08-03-02 v2.txt

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3 <110> APPLICANT: HSC Research and Development Limited Partnership
5 <120> TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
7 <130> FILE REFERENCE: 92906-2
9 <140> CURRENT APPLICATION NUMBER: US 09/600358A
10 <141> CURRENT FILING DATE: 2000-09-25
12 <150> PRIOR APPLICATION NUMBER: CA 2,220,853
13 <151> PRIOR FILING DATE: 1998-01-16
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: PatentIn Ver. 2.0
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20 <211> LENGTH: 3058
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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26 <222> LOCATION: (42)..(2465)
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31 1 5
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34 Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser Lys Lys Ile Thr Lys
35 10 15 20
37 gag gag ttt gcc aat gaa ttt ctg aag ctg aaa agg caa tct acc aag 152
38 Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys Arg Gln Ser Thr Lys
39 25 30 35
41 tac aag gca gac aaa acc tat cct aca act gtg gct gag aat gcc aag 200
42 Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val Ala Glu Asn Ala Lys
43 40 45 50
45 aat atc aag aaa aac aga tat aag gat att ttg ccc tat gat tat agc 248
46 Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu Pro Tyr Asp Tyr Ser
47 55 60 65
49 cgg gta gaa cta tcc ctg ata acc tct gat gag gat tcc agc tac atc 296
50 Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu Asp Ser Ser Tyr Ile
51 70 75 80 85
53 aat gcc aac ttc att aag gga gtt tat gga ccc aag gct tat att gcc 344
54 Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro Lys Ala Tyr Ile Ala
55 90 95 100
57 acc cag ggt cct tta tct aca acc ctc ctg gac ttc tgg agg atg att 392
58 Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp Phe Trp Arg Met Ile
59 105 110 115
61 tgg gaa tat agt gtc ctt atc att gtt atg gca tgc atg gag tat gaa 440
62 Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala Cys Met Glu Tyr Glu

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69	cag ctg gaa ttt ggc cct ttc tct gta tcc tgt gaa gct gaa aaa agg	536		
70	Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys Glu Ala Glu Lys Arg			
71	150	155	160	165
74	aaa tct gat tat ata atc agg act cta aaa gtt aag ttc aat agt gaa	584		
75	Lys Ser Asp Tyr Ile Arg Thr Leu Lys Val Lys Phe Asn Ser Glu			
76	170	175	180	
78	act cga act atc tac cag ttt cat tac aag aat tgg cca gac cat gat	632		
79	Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn Trp Pro Asp His Asp			
80	185	190	195	
82	gta cct tca tct ata gac cct att ctt gag ctc atc tgg gat gta cgt	680		
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84	200	205	210	
86	tgt tac caa gag gat gac agt gtt ccc ata tgc att cac tgc agt gct	728		
87	Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys Ile His Cys Ser Ala			
88	215	220	225	
90	ggc tgt gga agg act ggt gtt att tgt gct att gtt gat tat aca tgg	776		
91	Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile Val Asp Tyr Thr Trp			
92	230	235	240	245
94	atg ttg cta aaa gat ggg ata att cct gag aac ttc agt gtt ttc agt	824		
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96	250	255	260	
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102	gaa caa tat gaa ctg gtc tac aat gct gta tta gaa cta ttt aag aga	920		
103	Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu Glu Leu Phe Lys Arg			
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106	cag atg gat gtt atc aga gat aaa cat tct gga aca gag agt caa gca	968		
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108	295	300	305	
110	aag cat tgt att cct gag aaa aat cac act ctc caa gca gac tct tat	1016		
111	Lys His Cys Ile Pro Glu Lys Asn His Thr Leu Gln Ala Asp Ser Tyr			
112	310	315	320	325
114	tct cct aat tta cca aaa agt acc aca aaa gca gca aaa atg atg aac	1064		
115	Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala Ala Lys Met Met Asn			
116	330	335	340	
118	caa caa agg aca aaa atg gaa atc aaa gaa tct tct tcc ttt gac ttt	1112		
119	Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser Ser Ser Phe Asp Phe			
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122	agg act tct gaa ata agt gca aaa gaa gag cta gtt ttg cac cct gct	1160		
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126	aaa tca agc act tct ttt gac ttt ctg gag cta aat tac agt ttt gac	1208		
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132	390						395					400				405	
134	gtt	ggg	gag	cct	ctt	cag	aag	cat	caa	agt	ttg	gat	ttg	ggc	tct	ctt	1304
135	Val	Gly	Glu	Pro	Leu	Gln	Lys	His	Gln	Ser	Leu	Asp	Leu	Gly	Ser	Leu	
136					410					415					420		
139	ttg	ttt	gag	gga	tgt	tct	aat	tct	aaa	cct	gta	aat	gca	gca	gga	aga	1352
140	Leu	Phe	Glu	Gly	Cys	Ser	Asn	Ser	Lys	Pro	Val	Asn	Ala	Ala	Gly	Arg	
141				425					430						435		
143	tat	ttt	aat	tca	aag	gtg	cca	ata	aca	cgg	acc	aaa	tca	act	cct	ttt	1400
144	Tyr	Phe	Asn	Ser	Lys	Val	Pro	Ile	Thr	Arg	Thr	Lys	Ser	Thr	Pro	Phe	
145			440					445					450				
147	gaa	ttg	ata	cag	cag	aga	gaa	acc	aag	gag	gtg	gac	agc	aag	gaa	aac	1448
148	Glu	Leu	Ile	Gln	Gln	Arg	Glu	Thr	Lys	Glu	Val	Asp	Ser	Lys	Glu	Asn	
149		455				460						465					
151	ttt	tct	tat	ttg	gaa	tct	caa	cca	cat	gat	tct	tgt	ttt	gta	gag	atg	1496
152	Phe	Ser	Tyr	Leu	Glu	Ser	Gln	Pro	His	Asp	Ser	Cys	Phe	Val	Glu	Met	
153	470					475					480					485	
155	cag	gct	caa	aaa	gta	atg	cat	gtt	tct	tca	gca	gaa	ctg	aat	tat	tca	1544
156	Gln	Ala	Gln	Lys	Val	Met	His	Val	Ser	Ser	Ala	Glu	Leu	Asn	Tyr	Ser	
157				490						495					500		
159	ctg	cca	tat	gac	tct	aaa	cac	caa	ata	cgt	aat	gcc	tct	aat	gta	aag	1592
160	Leu	Pro	Tyr	Asp	Ser	Lys	His	Gln	Ile	Arg	Asn	Ala	Ser	Asn	Val	Lys	
161				505					510					515			
163	cac	cat	gac	tct	agt	gct	ctt	ggt	gta	tat	tct	tac	ata	cct	tta	gtg	1640
164	His	His	Asp	Ser	Ser	Ala	Leu	Gly	Val	Tyr	Ser	Tyr	Ile	Pro	Leu	Val	
165			520					525					530				
167	gaa	aat	cct	tat	ttt	tca	tca	tgg	cct	cca	agt	ggt	acc	agt	tct	aag	1688
168	Glu	Asn	Pro	Tyr	Phe	Ser	Ser	Trp	Pro	Pro	Ser	Gly	Thr	Ser	Ser	Lys	
169		535					540					545					
171	atg	tct	ctt	gat	tta	cct	gag	aag	caa	gat	gga	act	gtt	ttt	cct	tct	1736
172	Met	Ser	Leu	Asp	Leu	Pro	Glu	Lys	Gln	Asp	Gly	Thr	Val	Phe	Pro	Ser	
173	550					555					560					565	
175	tct	ctg	ttg	cca	aca	tcc	tct	aca	tcc	ctc	ttc	tct	tat	tac	aat	tca	1784
176	Ser	Leu	Leu	Pro	Thr	Ser	Ser	Thr	Ser	Leu	Phe	Ser	Tyr	Tyr	Asn	Ser	
177				570						575					580		
179	cat	agt	tct	tta	tca	ctg	aat	tct	cca	acc	aat	att	tcc	tca	cta	ttg	1832
180	His	Ser	Ser	Leu	Ser	Leu	Asn	Ser	Pro	Thr	Asn	Ile	Ser	Ser	Leu	Leu	
181				585					590						595		
183	aac	cag	gag	tca	gct	gta	cta	gca	act	gct	cca	agg	ata	gat	gat	gaa	1880
184	Asn	Gln	Glu	Ser	Ala	Val	Leu	Ala	Thr	Ala	Pro	Arg	Ile	Asp	Asp	Glu	
185		600						605					610				
187	atc	ccc	cct	cca	ctt	cct	gta	cgg	aca	cct	gaa	tca	ttt	att	gtg	gtt	1928
188	Ile	Pro	Pro	Pro	Leu	Pro	Val	Arg	Thr	Pro	Glu	Ser	Phe	Ile	Val	Val	
189		615					620					625					
191	gag	gaa	gct	gga	gaa	ttc	tca	cca	aat	gtt	ccc	aaa	tcc	tta	tcc	tca	1976
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193	630					635					640					645	
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200 Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu Arg Pro Ser Lys Ser
201                               665                               670                               675
204 gta aaa ctc cga agt cct aaa tca gaa cta cat caa gat cgt tct tct 2120
205 Val Lys Leu Arg Ser Pro Lys Ser Glu Leu His Gln Asp Arg Ser Ser
206                               680                               685                               690
208 ccc cca cct cct ctc cca gaa aga act cta gag tcc ttc ttt ctt gcc 2168
209 Pro Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser Phe Phe Leu Ala
210                               695                               700                               705
212 gat gaa gat tgt atg cag gcc caa tct ata gaa aca tat tct act agc 2216
213 Asp Glu Asp Cys Met Gln Ala Gln Ser Ile Glu Thr Tyr Ser Thr Ser
214 710                               715                               720                               725
216 tat cct gac acc atg gaa aat tca aca tct tca aaa cag aca ctg aag 2264
217 Tyr Pro Asp Thr Met Glu Asn Ser Thr Ser Ser Lys Gln Thr Leu Lys
218                               730                               735                               740
220 act cct gga aaa agt ttc aca agg agt aag agt ttg aaa att ttg cga 2312
221 Thr Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu Lys Ile Leu Arg
222                               745                               750                               755
224 aac atg aaa aag agt atc tgt aat tct tgc cca cca aac aag cct gca 2360
225 Asn Met Lys Lys Ser Ile Cys Asn Ser Cys Pro Pro Asn Lys Pro Ala
226                               760                               765                               770
228 gaa tct gtt cag tca aat aac tcc agc tca ttt ctg aat ttt ggt ttt 2408
229 Glu Ser Val Gln Ser Asn Asn Ser Ser Ser Phe Leu Asn Phe Gly Phe
230                               775                               780                               785
232 gca aac cgt ttt tca aaa ccc aaa gga cca agg aat cca cca cca act 2456
233 Ala Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro Pro Pro Thr
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237 Trp Asn Ile
239 acctgcaaact aaaactacta gaatactgct agttaaata agtgctctat atgcataata 2565
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243 gttttgcatt ttcatatcat ttgcattgag ttgaaaactg caaataaaag tttgtcactt 2685
245 gagcttatgt acagaatgct atatgagaaa cacttttaga atggatttat ttttcatttt 2745
247 tgccagttat ttttattttc ttttactttt ctacataaac ataaacttca aaagggtttgt 2805
249 aagattttgga tctcaactaa tttctacatt gccagaatat actataaaaaa gttaaaaaaa 2865
251 aaaacttact ttgtgggttg caatacaaac tgcctttgac aatgactatt ccctgacagt 2925
253 tatttttgcc taaatggagt ataccttgta aatcttccca aatgttgttg aaaactggaa 2985
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270 Lys Lys Ile Thr Lys Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys

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271			20				25				30					
273	Arg	Gln	Ser	Thr	Lys	Tyr	Lys	Ala	Asp	Lys	Thr	Tyr	Pro	Thr	Thr	Val
274			35				40				45					
276	Ala	Glu	Asn	Ala	Lys	Asn	Ile	Lys	Lys	Asn	Arg	Tyr	Lys	Asp	Ile	Leu
277		50				55					60					
279	Pro	Tyr	Asp	Tyr	Ser	Arg	Val	Glu	Leu	Ser	Leu	Ile	Thr	Ser	Asp	Glu
280	65				70					75					80	
282	Asp	Ser	Ser	Tyr	Ile	Asn	Ala	Asn	Phe	Ile	Lys	Gly	Val	Tyr	Gly	Pro
283				85					90					95		
285	Lys	Ala	Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Ser	Thr	Thr	Leu	Leu	Asp
286			100					105					110			
288	Phe	Trp	Arg	Met	Ile	Trp	Glu	Tyr	Ser	Val	Leu	Ile	Ile	Val	Met	Ala
289			115					120					125			
291	Cys	Met	Glu	Tyr	Glu	Met	Gly	Lys	Lys	Lys	Cys	Glu	Arg	Tyr	Trp	Ala
292		130					135					140				
294	Glu	Pro	Gly	Glu	Met	Gln	Leu	Glu	Phe	Gly	Pro	Phe	Ser	Val	Ser	Cys
295	145				150					155					160	
297	Glu	Ala	Glu	Lys	Arg	Lys	Ser	Asp	Tyr	Ile	Ile	Arg	Thr	Leu	Lys	Val
298				165					170					175		
300	Lys	Phe	Asn	Ser	Glu	Thr	Arg	Thr	Ile	Tyr	Gln	Phe	His	Tyr	Lys	Asn
301			180						185				190			
303	Trp	Pro	Asp	His	Asp	Val	Pro	Ser	Ile	Asp	Pro	Ile	Leu	Glu	Leu	
304		195					200					205				
306	Ile	Trp	Asp	Val	Arg	Cys	Tyr	Gln	Glu	Asp	Asp	Ser	Val	Pro	Ile	Cys
307		210				215					220					
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310	225				230					235					240	
312	Val	Asp	Tyr	Thr	Trp	Met	Leu	Leu	Lys	Asp	Gly	Ile	Ile	Pro	Glu	Asn
313				245					250					255		
315	Phe	Ser	Val	Phe	Ser	Leu	Ile	Arg	Glu	Met	Arg	Thr	Gln	Arg	Pro	Ser
316			260						265				270			
318	Leu	Val	Gln	Thr	Gln	Glu	Gln	Tyr	Glu	Leu	Val	Tyr	Asn	Ala	Val	Leu
319			275					280				285				
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322		290				295					300					
324	Thr	Glu	Ser	Gln	Ala	Lys	His	Cys	Ile	Pro	Glu	Lys	Asn	His	Thr	Leu
325	305				310					315					320	
327	Gln	Ala	Asp	Ser	Tyr	Ser	Pro	Asn	Leu	Pro	Lys	Ser	Thr	Thr	Lys	Ala
328				325					330					335		
330	Ala	Lys	Met	Met	Asn	Gln	Gln	Arg	Thr	Lys	Met	Glu	Ile	Lys	Glu	Ser
331			340					345				350				
334	Ser	Ser	Phe	Asp	Phe	Arg	Thr	Ser	Glu	Ile	Ser	Ala	Lys	Glu	Glu	Leu
335		355				360					365					
337	Val	Leu	His	Pro	Ala	Lys	Ser	Ser	Thr	Ser	Phe	Asp	Phe	Leu	Glu	Leu
338		370				375					380					
340	Asn	Tyr	Ser	Phe	Asp	Lys	Asn	Ala	Asp	Thr	Thr	Met	Lys	Trp	Gln	Thr
341	385				390					395					400	
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344				405					410					415		

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Seq#:3; Line(s) 546,547,548,549,550,551,552,553,554,555,556,557,558,559,560
Seq#:3; Line(s) 561,562,563,564,565,566,567,568,569,570,571,572,573,574,575
Seq#:3; Line(s) 576,577,578,579,580,581,582,583,584,585,586,587,588,589,590
Seq#:3; Line(s) 591,592,594,595,596,597,598,599,600,601,602,603,604,605,606
Seq#:3; Line(s) 607,608,609,610,611,612,613,614,615,616,617,618,619,620,621
Seq#:4; Line(s) 622,623,624,625,626,627,628,629,630,631,632,633,634,635,636
Seq#:4; Line(s) 637,638,639,640,641,642,643,644,645,646,647,648,649,650,651
Seq#:4; Line(s) 652,653,654,655,656,657,659,660,661,662,663,664,665,666,667

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/22/2002
PATENT APPLICATION: US/09/600,358A TIME: 13:23:41

Input Set : A:\92906-2 seq 08-03-02 v2.txt
Output Set: N:\CRF3\05222002\I600358A.raw

Seq#:4; Line(s) 668,669,670,671,672,673,674,675,676,677,678,679,680,681,682
Seq#:4; Line(s) 683,684,685,686,687,688,689,690,691,692,693,694,695,696,697
Seq#:4; Line(s) 698,699,700,701,702,703,704,705,706,707,708,709,710,711,712
Seq#:4; Line(s) 713,714,715,716,717,718,719,720,721,722,724,725,726,727,728
Seq#:4; Line(s) 729,730,731,732,733,734,735,736,737,738,739,740,741,742,743
Seq#:4; Line(s) 744,745,746,747,748,749,750,751,752,753,754,755,756,757,758
Seq#:4; Line(s) 759,760,761,762
Seq#:5; Line(s) 763,764,765,766,767,768,769,770,771,772,773,774,775,776,777
Seq#:5; Line(s) 778,779,780,781,782,783,784,785,786,787,789,790,791,792,793
Seq#:5; Line(s) 794,795,796,797,798,799,800,801,802,803,804,805,806,807,808
Seq#:5; Line(s) 809,810,811,812,813,814,815,816,817,818,819,820,821,822,823
Seq#:5; Line(s) 824,825,826,827,828,829,830,831,832,833,834,835,836,837,838
Seq#:5; Line(s) 839,840,841,842,843,844,845,846,847,848,849,850,851,852,854
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Seq#:5; Line(s) 900,901,902,903,904,905,906,907,908,909,910,911,912,913,914
Seq#:5; Line(s) 915,916,917,919,920,921,922,923,924,925
Seq#:6; Line(s) 926,927,928,929,930,931,932,933,934,935,936
Seq#:7; Line(s) 937,938,939,940,941,942,943

VERIFICATION SUMMARY

DATE: 05/22/2002

PATENT APPLICATION: US/09/600,358A

TIME: 13:23:41

Input Set : A:\92906-2 seq 08-03-02 v2.txt

Output Set: N:\CRF3\05222002\I600358A.raw